

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/041,859 A
Source: IFW16
Date Processed by STIC: 10/28/2005

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 10/28/2005

PATENT APPLICATION: US/10/041,859A

TIME: 10:48:08

Input Set : A:\101602np.app

Output Set: N:\CRF4\10282005\J041859A.raw

3 <110> APPLICANT: HUANG, QIHONG
 4 REED, JOHN C.
 5 DEVERAUX, QUINN L.
 6 MAEDA, SUSUMU
 8 <120> TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND
 9 METHODS FOR MAKING AND USING THEM
 11 <130> FILE REFERENCE: 087102/027 2537
 13 <140> CURRENT APPLICATION NUMBER: 10/041,859A
 14 <141> CURRENT FILING DATE: 2002-01-07
 16 <150> PRIOR APPLICATION NUMBER: 60/260,478
 17 <151> PRIOR FILING DATE: 2001-01-08
 19 <160> NUMBER OF SEQ ID NOS: 27
 21 <170> SOFTWARE: PatentIn Ver. 3.3
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 3773
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Bombyx mori
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (2733)..(3770)
 32 <400> SEQUENCE: 1
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 37 ttcttgcaag acgagtgctca gtgattaaac aaaaacataa gaatagacgt tttatgcggt 180
 39 actaaaaaaaa aggaaaaata taccaatgga gttgacgaaa gttgctaaaa atggagctgc 240
 41 cgccacgttg gtgatgttaa aaaatgcgcg ggatgcaaaa atgcgacctt tcattgggtcc 300
 43 gctcatgtta tcctcgtgtg agtcttcaac gacatccaca ctcccgtcac cttcgtcgtc 360
 45 agctgataaa acggataatc acgacacatt caacttcctt cctgatatgc ccgacatgcg 420
 47 tcgtgaagag gaacgtctga aaacatttga tcagtggccc gttacgtttt tgacgccgga 480
 49 acaattggcc cgcaacggat tctactacct cggtcgcggc gacgaagtgt gctgtgcttt 540
 51 ctgtaaggta gaaattatga ggtgggtcga aggcgacgat cctgccgccg atcatcggag 600
 53 atgggcgccc cagtgtccct ttgtacgaaa acaaagtgtat gccaacgctg ggggagaggc 660
 55 gaccgctgtc ggtagagacg aatgtggggc cagtgcggcc acgcagcctc cccgcatgcc 720
 57 cggccccgtg cacgcgcggt actccaccga ggccgcgcgg ctccgccacct tcaaggactg 780
 59 gccgagacgt atgcgccaaa aacccgagga actggcagag gccggattct tctatacagg 840
 61 ccaaggtgac aaaacgaaat gcttctattg cgacggaggg ctaaaagatt gggaaaagcga 900
 63 tgacgttccg tgggaacagc acgccagatg gttcgaccgc tgcgcgtacg tgcaattggt 960
 65 gaaaggacgt gactacattc agaaggtgaa gtcggaggcc actgcgatat ctgctagcga 1020
 67 agaagaacag gccgccacca atgattcgac taagaacgtc gcccaagagg gcgagaaaca 1080
 69 tttggatgac tctaaaatat gtaaaatatg ttattccgag gagcgtaacg tgtgcttcgt 1140
 71 gccgtgcggc cacgtgggtg cgtgcgccaa gtgcgcgctg tcgacggaca agtgcccgat 1200
 73 gtgtcgcagg acgttcacga atgcgggtgc gctctacttc tcgtgaaagg accctcctcg 1260
 75 cgagctgtat actaatcact tcaccgggag gccctggagc gtgctgaaac cacccttcga 1320

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77 acgaaaccgc gtatcctgtg atttttacat taaataaatt tacaaattga tagcgggtggg 1380
79 gcaatgtata ggaactcgtc agaactcgcg agttgacgtg caggaaggag ttagtgattt 1440
81 gtaaacttgt aaactgatgt tgaaatgatt ttattttatta tttaaaattc taatgacaaa 1500
83 gtgtaagtaa ataaatgtac atattatttt agattatcag tttgtccac cgacaaaagt 1560
85 gaaatgtaca taggtgtttt catatcactt caacagtcga agaccttctt tttgaattta 1620
87 aggatatata tttatacata taaattaaaa ttttaacgag acatcaatat aaatgggttta 1680
89 acaacttatt tatacactga aatcaagtga agtgtaacat ggtctgaaga atgttttact 1740
91 gattttcactt cccctgttga agtgataaaa ttctaagtga aatccagagt ttaaagtgcg 1800
93 tcataattaa tataagaaac aagttttacg cttcttttgc ttgaaaaatc ttataattga 1860
95 ttcaggaatt atttaagtgt actatatttt gttcctgtaa ataacataat atatactatt 1920
97 tattgattaa ttctgacata atttatggca attccgtaag atacaatcca atacttattt 1980
99 catgtaactc acttcaaaat agttgaatgt gtggtgtgat tataatgtta aatgtctaaa 2040
101 tttataataa attgagcaaa gttgcattta atgtatgaat actaattatt gttttaacaa 2100
103 aacattttaag tataatctgc tctgtgattt taatgtatca agaaataacc ccaacacctt 2160
105 aattgaagtt tttacattgt tgctgataaa aaaaatcata tcaattacat ttacaagtca 2220
107 attttaattg ttcagaaacc aaacacaatt ttgttagtga ctcttgcttt acgaagtagt 2280
109 atgacaaacc agtgtttcgt tgattgcatt aatttagttg taaccaatat ttacactcaa 2340
111 cattttaaga tgcatttgag gaattctgta taaaaaatgg gaatttattt attggtgtat 2400
113 aatacaatcc cgcacaagcc atttgcaagt ttctacacaa ctaaaacgta ttgtatccat 2460
115 tatctatacg tcatatcatt aatatatact tgcttttagca aacatatatt cacgaataac 2520
117 ttcacaatat atttttgtaa atcaacatat taatggtaat taacgaatcg cacggtacaa 2580
119 atagtataaa ctgctgagtg cactaaatag taagagaatt tatttaacaa gtcaaatatt 2640
121 gtttcataag tagttatttc atactgttga atgttattca ttaaaacaaa tgttaaagca 2700
123 aaaaaaaaaa aaaaaagtcg tgactgggaa aa atg gag ttg acg aaa gtt gct 2753
124 Met Glu Leu Thr Lys Val Ala
125 1 5
127 aaa aat gga gct gcc gcc acg ttg gtg atg tta aaa aat gcg cgg gat 2801
128 Lys Asn Gly Ala Ala Ala Thr Leu Val Met Leu Lys Asn Ala Arg Asp
129 10 15 20
131 gca aaa atg cga cct ttc att ggt ccg ctc atg tta tcc tcg tgt gag 2849
132 Ala Lys Met Arg Pro Phe Ile Gly Pro Leu Met Leu Ser Ser Cys Glu
133 25 30 35
135 tct tca acg aca tcc aca ctc ccg tca cct tcg tcg tca gct gat aaa 2897
136 Ser Ser Thr Thr Ser Thr Leu Pro Ser Pro Ser Ser Ser Ala Asp Lys
137 40 45 50 55
139 acg gat aat cac gac aca ttc aac ttc ctt cct gat atg ccc gac atg 2945
140 Thr Asp Asn His Asp Thr Phe Asn Phe Leu Pro Asp Met Pro Asp Met
141 60 65 70
143 cgt cgt gaa gag gaa cgt ctg aaa aca ttt gat cag tgg ccc gtt acg 2993
144 Arg Arg Glu Glu Glu Arg Leu Lys Thr Phe Asp Gln Trp Pro Val Thr
145 75 80 85
147 ttt ttg acg ccg gaa caa ttg gcc cgc aac gga ttc tac tac ctc ggt 3041
148 Phe Leu Thr Pro Glu Gln Leu Ala Arg Asn Gly Phe Tyr Tyr Leu Gly
149 90 95 100
151 cgc ggc gac gaa gtg tgc tgt gct ttc tgt aag gta gaa att atg agg 3089
152 Arg Gly Asp Glu Val Cys Cys Ala Phe Cys Lys Val Glu Ile Met Arg
153 105 110 115
155 tgg gtc gaa ggc gac gat cct gcc gcc gat cat cgg aga tgg gcg ccc 3137
156 Trp Val Glu Gly Asp Asp Pro Ala Ala Asp His Arg Arg Trp Ala Pro

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157 120          125          130          135
159 cag tgt ccc ttt gta cga aaa caa atg tat gcc aac gct ggg gga gag 3185
160 Gln Cys Pro Phe Val Arg Lys Gln Met Tyr Ala Asn Ala Gly Gly Glu
161          140          145          150
163 gcg acc gct gtc ggt aga gac gaa tgt ggg gcc agt gcg gcc acg cag 3233
164 Ala Thr Ala Val Gly Arg Asp Glu Cys Gly Ala Ser Ala Ala Thr Gln
165          155          160          165
167 cct ccc cgc atg ccc ggc ccc gtg cac gcg cgg tac tcc acc gag gcc 3281
168 Pro Pro Arg Met Pro Gly Pro Val His Ala Arg Tyr Ser Thr Glu Ala
169          170          175          180
171 gcg cgg ctc gcc acc ttc aag gac tgg ccg aga cgt atg cgc caa aaa 3329
172 Ala Arg Leu Ala Thr Phe Lys Asp Trp Pro Arg Arg Met Arg Gln Lys
173          185          190          195
175 ccc gag gaa ctg gca gag gcc gga ttc ttc tat aca ggc caa ggt gac 3377
176 Pro Glu Glu Leu Ala Glu Ala Gly Phe Phe Tyr Thr Gly Gln Gly Asp
177 200          205          210          215
179 aaa acg aaa tgc ttc tat tgc gac gga ggg cta aaa gat tgg gaa agc 3425
180 Lys Thr Lys Cys Phe Tyr Cys Asp Gly Gly Leu Lys Asp Trp Glu Ser
181          220          225          230
183 gat gac gtt ccg tgg gaa cag cac gcc aga tgg ttc gac cgc tgc gcg 3473
184 Asp Asp Val Pro Trp Glu Gln His Ala Arg Trp Phe Asp Arg Cys Ala
185          235          240          245
187 tac gtg caa ttg gtg aaa gga cgt gac tac att cag aag gtg aag tcg 3521
188 Tyr Val Gln Leu Val Lys Gly Arg Asp Tyr Ile Gln Lys Val Lys Ser
189          250          255          260
191 gag gcc act gcg ata tct gct agc gaa gaa gaa cag gcc gcc acc aat 3569
192 Glu Ala Thr Ala Ile Ser Ala Ser Glu Glu Glu Gln Ala Ala Thr Asn
193          265          270          275
195 gat tcg act aag aac gtc gcc caa gag ggc gag aaa cat ttg gat gac 3617
196 Asp Ser Thr Lys Asn Val Ala Gln Glu Gly Glu Lys His Leu Asp Asp
197 280          285          290          295
199 tct aaa ata tgt aaa ata tgt tat tcc gag gag cgt aac gtg tgc ttc 3665
200 Ser Lys Ile Cys Lys Ile Cys Tyr Ser Glu Glu Arg Asn Val Cys Phe
201          300          305          310
203 gtg ccg tgc ggc cac gtg gtg gcg tgc gcc aag tgc gcg ctg tcg acg 3713
204 Val Pro Cys Gly His Val Val Ala Cys Ala Lys Cys Ala Leu Ser Thr
205          315          320          325
207 gac aag tgc ccg atg tgt cgc agg acg ttc acg aat gcg gtg cgg ctc 3761
208 Asp Lys Cys Pro Met Cys Arg Arg Thr Phe Thr Asn Ala Val Arg Leu
209          330          335          340
211 tac ttc tcg tga 3773
212 Tyr Phe Ser
213          345
216 <210> SEQ ID NO: 2
217 <211> LENGTH: 346
218 <212> TYPE: PRT
219 <213> ORGANISM: Bombyx mori
221 <400> SEQUENCE: 2
222 Met Glu Leu Thr Lys Val Ala Lys Asn Gly Ala Ala Ala Thr Leu Val

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223      1              5              10              15
225 Met Leu Lys Asn Ala Arg Asp Ala Lys Met Arg Pro Phe Ile Gly Pro
226              20              25              30
228 Leu Met Leu Ser Ser Cys Glu Ser Thr Thr Ser Thr Leu Pro Ser
229              35              40              45
231 Pro Ser Ser Ser Ala Asp Lys Thr Asp Asn His Asp Thr Phe Asn Phe
232              50              55              60
234 Leu Pro Asp Met Pro Asp Met Arg Arg Glu Glu Glu Arg Leu Lys Thr
235      65              70              75              80
237 Phe Asp Gln Trp Pro Val Thr Phe Leu Thr Pro Glu Gln Leu Ala Arg
238              85              90              95
240 Asn Gly Phe Tyr Tyr Leu Gly Arg Gly Asp Glu Val Cys Cys Ala Phe
241              100             105             110
243 Cys Lys Val Glu Ile Met Arg Trp Val Glu Gly Asp Asp Pro Ala Ala
244              115             120             125
246 Asp His Arg Arg Trp Ala Pro Gln Cys Pro Phe Val Arg Lys Gln Met
247      130             135             140
249 Tyr Ala Asn Ala Gly Gly Glu Ala Thr Ala Val Gly Arg Asp Glu Cys
250 145             150             155             160
252 Gly Ala Ser Ala Ala Thr Gln Pro Pro Arg Met Pro Gly Pro Val His
253              165             170             175
255 Ala Arg Tyr Ser Thr Glu Ala Ala Arg Leu Ala Thr Phe Lys Asp Trp
256              180             185             190
258 Pro Arg Arg Met Arg Gln Lys Pro Glu Glu Leu Ala Glu Ala Gly Phe
259              195             200             205
261 Phe Tyr Thr Gly Gln Gly Asp Lys Thr Lys Cys Phe Tyr Cys Asp Gly
262      210             215             220
264 Gly Leu Lys Asp Trp Glu Ser Asp Asp Val Pro Trp Glu Gln His Ala
265 225             230             235             240
267 Arg Trp Phe Asp Arg Cys Ala Tyr Val Gln Leu Val Lys Gly Arg Asp
268              245             250             255
270 Tyr Ile Gln Lys Val Lys Ser Glu Ala Thr Ala Ile Ser Ala Ser Glu
271              260             265             270
273 Glu Glu Gln Ala Ala Thr Asn Asp Ser Thr Lys Asn Val Ala Gln Glu
274      275             280             285
276 Gly Glu Lys His Leu Asp Asp Ser Lys Ile Cys Lys Ile Cys Tyr Ser
277      290             295             300
279 Glu Glu Arg Asn Val Cys Phe Val Pro Cys Gly His Val Val Ala Cys
280 305             310             315             320
282 Ala Lys Cys Ala Leu Ser Thr Asp Lys Cys Pro Met Cys Arg Arg Thr
283              325             330             335
285 Phe Thr Asn Ala Val Arg Leu Tyr Phe Ser
286              340             345
289 <210> SEQ ID NO: 3
290 <211> LENGTH: 20
291 <212> TYPE: DNA
292 <213> ORGANISM: Artificial Sequence
294 <220> FEATURE:
295 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

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297 <220> FEATURE:
298 <221> NAME/KEY: modified_base
299 <222> LOCATION: (3)
300 <223> OTHER INFORMATION: a, c, g or t
302 <220> FEATURE:
303 <221> NAME/KEY: modified_base
304 <222> LOCATION: (6)
305 <223> OTHER INFORMATION: a, c, g or t
307 <220> FEATURE:
308 <221> NAME/KEY: modified_base
309 <222> LOCATION: (9)
310 <223> OTHER INFORMATION: a, c, g or t
312 <220> FEATURE:
313 <221> NAME/KEY: modified_base
314 <222> LOCATION: (12)
315 <223> OTHER INFORMATION: a, c, g or t
317 <400> SEQUENCE: 3
W--> 318 gcngangcng gnttyttyta 20
321 <210> SEQ ID NO: 4
322 <211> LENGTH: 17
323 <212> TYPE: DNA
324 <213> ORGANISM: Artificial Sequence
326 <220> FEATURE:
327 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer
329 <220> FEATURE:
330 <221> NAME/KEY: modified_base
331 <222> LOCATION: (3)
332 <223> OTHER INFORMATION: a, c, g or t
334 <220> FEATURE:
335 <221> NAME/KEY: modified_base
336 <222> LOCATION: (9)
337 <223> OTHER INFORMATION: a, c, g or t
339 <220> FEATURE:
340 <221> NAME/KEY: modified_base
341 <222> LOCATION: (15)
342 <223> OTHER INFORMATION: a, c, g or t
344 <400> SEQUENCE: 4
W--> 345 acnacrtgnc crcangg 17
348 <210> SEQ ID NO: 5
349 <211> LENGTH: 18
350 <212> TYPE: DNA
351 <213> ORGANISM: Artificial Sequence
353 <220> FEATURE:
354 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer
356 <400> SEQUENCE: 5
357 ctgttccac ggaacgtc 18
360 <210> SEQ ID NO: 6
361 <211> LENGTH: 17
362 <212> TYPE: DNA

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/041,859A

DATE: 10/28/2005
TIME: 10:48:09

Input Set : A:\101602np.app
Output Set: N:\CRF4\10282005\J041859A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 3,6,9,12

Seq#:4; N Pos. 3,9,15

Seq#:7; Xaa Pos. 2,3,5,6,7,8,9,10,12,13,14,15,16,17,18,19,20,22,23,24,25,26

Seq#:7; Xaa Pos. 27

VERIFICATION SUMMARY

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Input Set : A:\101602np.app

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L:318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:345 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:402 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0
L:405 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:16